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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/736,960

DATE: 10/04/2001
 TIME: 17:50:41

Input Set : A:\-5-1-1.app
 Output Set: N:\CRF3\10042001\I736960.raw

3 <110> APPLICANT: In. Peter
 4 Garman, Jonathan David
 5 Candia III, Albert Frederick
 6 Arbor Vita Corporation
 8 <120> TITLE OF INVENTION: CLASP-5 Transmembrane Protein
 10 <130> FILE REFERENCE: 020054-000511US
 12 <140> CURRENT APPLICATION NUMBER: US 09/736,960
 C--> 13 <141> CURRENT FILING DATE: 2001-09-20
 15 <150> PRIOR APPLICATION NUMBER: US 60/160,860
 16 <151> PRIOR FILING DATE: 1999-10-21
 18 <150> PRIOR APPLICATION NUMBER: US 60/162,498
 19 <151> PRIOR FILING DATE: 1999-10-29
 21 <150> PRIOR APPLICATION NUMBER: US 60/170,453
 22 <151> PRIOR FILING DATE: 1999-12-13
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 25 <151> PRIOR FILING DATE: 2000-01-14
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 45 <150> PRIOR APPLICATION NUMBER: US 09/687,837
 46 <151> PRIOR FILING DATE: 2000-10-13
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 58 <151> PRIOR FILING DATE: 2000-10-13
 60 <160> NUMBER OF SEQ ID NOS: 134
 62 <170> SOFTWARE: PatentIn Ver. 2.1
 64 <210> SEQ ID NO: 1
 65 <211> LENGTH: 7215
 66 <212> TYPE: DNA

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75 <223> OTHER INFORMATION: human CLASP-5
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81 Met Thr
82 1
84 cac ctg aac agc ctg gat gtg cag ctt gcc cag gag ctc ggg gac ttc 165
85 His Leu Asn Ser Leu Asp Val Gln Leu Ala Gln Glu Leu Gly Asp Phe
86 5 10 15
88 act gat gac gac ttg gac gtg gtg ttc acg cca aag gaa tgt agg act 213
89 Thr Asp Asp Asp Leu Asp Val Val Phe Thr Pro Lys Glu Cys Arg Thr
90 20 25 30
92 ttg cag ccc tct ttg ccg qag qaa qqq qtt qaa ctg gac cct cat qtc 261
93 Leu Gln Pro Ser Leu Pro Glu Glu Gly Val Glu Leu Asp Pro His Val
94 35 40 45 50
96 agg gac tgt qtt cag acc tac atc cgt gag tgg cta atc gtg aac cgg 309
97 Arg Asp Cys Val Gln Thr Tyr Ile Arg Glu Trp Leu Ile Val Asn Arg
98 55 60 65
100 aaa aac caa gga agt cca gaa atc tgt gcc ttt aaa aag act gga tct 357
101 Lys Asn Gln Gly Ser Pro Glu Ile Cys Gly Phe Lys Lys Thr Gly Ser
102 70 75 80
104 cga aaa gat ttt cac aag acg ctt ccg aaa cag acg ttt gag tgg gaa 405
105 Arg Lys Asp Phe His Lys Thr Leu Pro Lys Gln Thr Phe Glu Ser Glu
106 85 90 95
108 acc ttg gag tgc agt gaa ccc gct gct cag gca ggc ccc cgc cac tta 453
109 Thr Leu Glu Cys Ser Glu Pro Ala Ala Gln Ala Gly Pro Arg His Leu
110 100 105 110
112 aac gtg ctg tgc gac gtg tct ggg aaa ggc ccc gtc act gcc tgt gac 501
113 Asn Val Leu Cys Asp Val Ser Gly Lys Gly Pro Val Thr Ala Cys Asp
114 115 120 125 130
116 ttt gac ctc cgc agc ctg cag cct gac aag cgg cta gaa aac ctc ctg 549
117 Phe Asp Leu Arg Ser Leu Gln Pro Asp Lys Arg Leu Glu Asn Leu Leu
118 135 140 145
120 cag caa gtg agt gcc gag gac ttt gag aag cag aac qag gag gcc cgg 597
121 Gln Gln Val Ser Ala Glu Asp Phe Glu Lys Gln Asn Glu Glu Ala Arg
122 150 155 160
124 aag acc aac agg cag gcc gag ctc ttt gcc ctt tac cca tca gtg gac 645
125 Arg Thr Asn Arg Gln Ala Glu Leu Phe Ala Leu Tyr Pro Ser Val Asp
126 165 170 175
128 gag gaa gat gct gtg gaa ata cgt cca gta cca gaa tgt ccc aag gaa 693
129 Glu Glu Asp Ala Val Glu Ile Arg Pro Val Pro Glu Cys Pro Lys Glu
130 180 185 190
132 cac ctg gcc aac aqa ata ttg gtc aag ttg cta acc tta aag ttc qag 741
133 His Leu Gly Asn Arg Ile Leu Val Lys Leu Leu Thr Leu Lys Phe Glu
134 195 200 205 210
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141 Glu Arg Lys Lys Ile Ser Glu Asn Phe His Cys Asp Leu Asn Ser Asp				
142	230	235	240	
144 cag ttc aaa gga ttt ctg cga gct cag acg cct tca gtg gcc gca tca				885
145 Gln Phe Lys Gly Phe Leu Arg Ala His Thr Pro Ser Val Ala Ala Ser				
146	245	250	255	
148 agt cag gcg aga tct gca gtc ttc tca gtc acc tac ccg tcc tca gac				933
149 Ser Gln Ala Arg Ser Ala Val Phe Ser Val Thr Tyr Pro Ser Ser Asp				
150	260	265	270	
152 atc tac ctg gta gtc aag att gaa aaa gtc ctg cag cag gga gat att				981
153 Ile Tyr Leu Val Val Lys Ile Glu Lys Val Leu Gln Gln Gly Asp Ile				
154 275	280	285	290	
156 gga gac tgt gca gag ccc tac acg gtt atc aaa gaa agt gat ggt gga				1029
157 Gly Asp Cys Ala Glu Pro Tyr Thr Val Ile Lys Glu Ser Asp Gly Gly				
158	295	300	305	
160 aag agt aaa gaa aag att gaa aaa cta aaa ctc caa gct gaa tcc ttc				1077
161 Lys Ser Lys Glu Lys Ile Glu Lys Leu Lys Leu Gln Ala Glu Ser Phe				
162	310	315	320	
164 tgc cag cgt ttg ggg aaa tac cgg atg ccc ttt gcc tgg gca ccc ata				1125
165 Cys Gln Arg Leu Gly Lys Tyr Arg Met Pro Phe Ala Trp Ala Pro Ile				
166	325	330	335	
168 agc tta tca agc ttc ttc aat gtc tcc acc ctt gag agg gag gta act				1173
169 Ser Leu Ser Ser Phe Phe Asn Val Ser Thr Leu Glu Arg Glu Val Thr				
170	340	345	350	
172 gat gtg gac tct gtg gtt ggg aga agc cca gtg ggt gaa cgg agg aca				1221
173 Asp Val Asp Ser Val Val Gly Arg Ser Pro Val Gly Glu Arg Arg Thr				
174 355	360	365	370	
176 ttg gcc caa tct aga agg ctt tct gaa aga gcc ctc tcc ttg gag gaa				1269
177 Leu Ala Gln Ser Arg Arg Leu Ser Glu Arg Ala Leu Ser Leu Glu Glu				
178	375	380	385	
180 aat ggg gtt gga tcc aac ttc aaa acc tcc act ctg agc gtt agc agc				1317
181 Asn Gly Val Gly Ser Asn Phe Lys Thr Ser Thr Leu Ser Val Ser Ser				
182	390	395	400	
184 ttt ttc aag cag gaa gga gat cgc ctt agc gat gaa gac tta ttc aag				1365
185 Phe Phe Lys Gln Glu Gly Asp Arg Leu Ser Asp Glu Asp Leu Phe Lys				
186	405	410	415	
188 ttt tta gct gac tac aaa aga tca tca tcc tta cag aqa cga gtc aag				14 3
189 Phe Leu Ala Asp Tyr Lys Arg Ser Ser Ser Leu Gln Arg Arg Val Lys				
190	420	425	430	
192 tca att cca ggc ttg cta aqa ctg gaa att tct aca gct cca gaa atc				1461
193 Ser Ile Pro Gly Leu Leu Arg Leu Glu Ile Ser Thr Ala Pro Glu Ile				
194 435	440	445	450	
196 atc aat tgc tat ctg act cct gaa atg ctg ccc gtg aaa ccc ttt cct				1509
197 Ile Asn Cys Cys Leu Thr Pro Glu Met Leu Pro Val Lys Pro Phe Pro				
198	455	460	465	
200 gaa aac cag aca cgc ccg cac aaa gaa att ttg gaa ttt cca aca cga				1557
201 Gln Asn Tyr Phe Arg Asp His Leu Ala Ile Thr Thr Thr Phe Phe Thr Thr				

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204	gaa gta tat gtc cct cac act gtg tac aqa aac ctt ctc tat gtc tac	1605
205	Glu Val Tyr Val Pro His Thr Val Tyr Arg Asn Leu Leu Tyr Val Tyr	
206	485 490 495	
208	cca caq agg ctg aac ttt gta aac aaa cta gca tca gcc cgg aac att	1653
209	Pro Gln Arg Leu Asn Phe Val Asn Lys Leu Ala Ser Ala Arg Asn Ile	
210	500 505 510	
212	aca ata aag atc cag ttt atg tgt gga gaa gat gct agc aat gcg atg	1701
213	Thr Ile Lys Ile Gln Phe Met Cys Gly Glu Asp Ala Ser Asn Ala Met	
214	515 520 525 530	
216	ccg gtc atc ttt gga aaa tcc agc ggg cct gaa ttt ctg cag gaa gtg	1749
217	Pro Val Ile Phe Gly Lys Ser Ser Gly Pro Glu Phe Leu Gln Glu Val	
218	535 540 545	
220	tac aca gct gtt aca tac cat aat aag tct cct gac ttt tat gaa gaa	1797
221	Tyr Thr Ala Val Thr Tyr His Asn Lys Ser Pro Asp Phe Tyr Glu Glu	
222	550 555 560	
224	gtg aaa att aag ctc ccc gct aag ctc aca gta aat cac cac ctc ctg	1845
225	Val Lys Ile Lys Leu Pro Ala Lys Leu Thr Val Asn His His Leu Leu	
226	565 570 575	
228	ttc acc ttc tac cat atc agc tgt cag cag aag caa gga gcc tcc gtg	1893
229	Phe Thr Phe Tyr His Ile Ser Cys Gln Gln Lys Gln Gly Ala Ser Val	
230	580 585 590	
232	gaa act ctc ctg gga tat tca tgg ctg cca att ctc tta aat gaa cgt	1941
233	Glu Thr Leu Leu Gly Tyr Ser Trp Leu Pro Ile Leu Leu Asn Glu Arg	
234	595 600 605 610	
236	ctt caa act gga tcc tac tgt ctc cca gtt gcc ttg gaa aaa ttg cca	1989
237	Leu Gln Thr Gly Ser Tyr Cys Leu Pro Val Ala Leu Glu Lys Leu Pro	
238	615 620 625	
240	ccc aac tac tcc atg cat tct gct gag aaa gtc cca tta cag aat cct	2037
241	Pro Asn Tyr Ser Met His Ser Ala Glu Lys Val Pro Leu Gln Asn Pro	
242	630 635 640	
244	ccc att aag tgg gct gaa gga cat aag gga gta ttt aat att gaa gtg	2085
245	Pro Ile Lys Trp Ala Glu Gly His Lys Gly Val Phe Asn Ile Glu Val	
246	645 650 655	
248	caa gct gtt tct tct gta cac acc caq gac aac cac ctg qag aag ttc	2133
249	Gln Ala Val Ser Ser Val His Thr Gln Asp Asn His Leu Glu Lys Phe	
250	660 665 670	
252	ttc acc ctc tgc cac tcc ctg gag agc cag gtg acc ttc ccc atc cgc	2181
253	Phe Thr Leu Cys His Ser Leu Glu Ser Gln Val Thr Phe Pro Ile Arg	
254	675 680 685 690	
256	gtg ctg gat caq aaa atc agc gag atg ccg ctg gag cat gag ctg aag	2229
257	Val Leu Asp Gln Lys Ile Ser Glu Met Ala Leu Glu His Glu Leu Lys	
258	695 700 705	
260	ctc agc atc atc tgc ctg aac tcc tcc cgc ctg gag ccg ctc gtg ctc	2277
261	Leu Ser Ile Ile Cys Leu Asn Ser Ser Arg Leu Glu Pro Leu Val Leu	
262	710 715 720	
264	ttc ctg cac ctg gtg ctg gac aag ctc ttc cag ctg tcc gtg cag ccc	2325
265	Phe Leu His Leu Val Leu Asp Lys Leu Phe Gln Leu Ser Val Gln Pro	
266	725 730 735	

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PATENT APPLICATION: US/09/736,960

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Input Set : A:\-5-1-1.app

Output Set: N:\CRF3\10042001\I736960.raw

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272 tcc gtg gtg gcc atc gcc aac agt ctg cac aac agc aag gac ctg agc 2421
273 Ser Val Val Ala Ile Ala Asn Ser Leu His Asn Ser Lys Asp Leu Ser
274 755      760      765      770
276 aag gac cag cat ggg agg aac tgc ctg ctg gcc tcc ttc gty cac tac 2469
277 Lys Asp Gln His Gly Arg Asn Cys Leu Leu Ala Ser Tyr Val His Tyr
278      775      780      785
280 gtc ttc cgc ctg cca gag gtg caa agg gat gtg ccc aag tca gcc gct 2517
281 Val Phe Arg Leu Pro Glu Val Gln Arg Asp Val Pro Lys Ser Gly Ala
282      790      795      800
284 ccc act gcc ctc cta gac cct cgg agc tac cac acg tat gcc cgc aca 2565
285 Pro Thr Ala Leu Leu Asp Pro Arg Ser Tyr His Thr Tyr Gly Arg Thr
286      805      810      815
288 tca gct gct gct gtg agt tca aag ctg ctg caa gcc cgg ttg atg agc 2613
289 Ser Ala Ala Ala Val Ser Ser Lys Leu Leu Gln Ala Arg Val Met Ser
290      820      825      830
292 agc agt aac cca gac ctc ggg ggg aca cac tcc caa gca gac gag gaa 2661
293 Ser Ser Asn Pro Asp Leu Ala Gly Thr His Ser Ala Ala Asp Glu Glu
294 835      840      845      850
296 gtg aag aac atc atg tct tca aag atc gcc gat cgc aac tgc agc cga 2709
297 Val Lys Asn Ile Met Ser Ser Lys Ile Ala Asp Arg Asn Cys Ser Arg
298      855      860      865
300 atg tct tac tat tgc tct ggc agt agt gat gct cca agt tca cct gca 2757
301 Met Ser Tyr Tyr Cys Ser Gly Ser Ser Asp Ala Pro Ser Ser Pro Ala
302      870      875      880
304 gcc cca agg cca gcc agc aaa aag cat ttc cat gag gag att gcc att 2805
305 Ala Pro Arg Pro Ala Ser Lys Lys His Phe His Glu Glu Leu Ala Leu
306      885      890      895
308 cag atg gtg gtc agc acc gga atg gtg aaa agc atg gcc cag cac gta 2853
309 Gln Met Val Val Ser Thr Gly Met Val Lys Ser Met Ala Gln His Val
310      900      905      910
312 cat aac atg gac aaa cgg gac agt ttt cgg agg act cct ttt tct gac 2901
313 His Asn Met Asp Lys Arg Asp Ser Phe Arg Arg Thr Arg Phe Ser Asp
314 915      920      925      930
316 cgt ttc atg gat gac ata act act att gtt aat ttg gtc acc tcg gaa 2949
317 Arg Phe Met Asp Asp Ile Thr Thr Ile Val Asn Val Val Thr Ser Glu
318      935      940      945
320 att gta gcc ctt tta gta aac cca cag aag gaa aat gaa cag ggg gaa 2997
321 Ile Ala Ala Leu Leu Val Lys Pro Gln Lys Glu Asn Glu Gln Ala Glu
322      950      955      960
324 aag atg aac atc agc ctg gct ttc ttc ttg tat gac att ctc tcc ctc 3045
325 Lys Met Asn Ile Ser Leu Ala Phe Phe Leu Tyr Asp Leu Leu Ser Leu
326      965      970      975
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329 Met Asp Arg Gly Phe Val Phe Asn Leu Ile Arg His Tyr Cys Ser Gln
330      980      985      990
332 ctg tca gcc aag ctc agt tgc att cca agc ctc att tca tta gaa caa 3111

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Sequence listing in accordance with the requirements of the patent laws of the United States and the European Patent Convention to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence listing page.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/736,960

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L:1275 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:1279 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
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 L:8194 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (104) SEQUENCE:
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 L:8242 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (112) SEQUENCE:
 L:8248 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (113) SEQUENCE:
 L:8254 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (114) SEQUENCE:
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 L:8272 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (117) SEQUENCE:
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